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G1071 (95)
T06584 (102)
SAP1 (103)
G1072 (96)
AAK00433 (104)
G1068 (97)
G1069 (42)
G2153 (6)
G3456 (14)
G3401 (38)
G3402 (101)
G3403 (22)
G2157 (98)
G3556 (40)
G1067 (4)
G2156 (8)
G3400 (30)
G3399 (10)
G1073 (2)
G2789 (99)
G596 (100)
G1070 (48)
G3405 (28)
G3404 (32)
G1075 (54)
G1076 (54)
G3460 (18)
G3459 (16)
G3458 (24)
G3406 (26)
G3407 (34)
G1945 (44)
G2155 (46)
G3408 (20)
BAB64709 (105)
G3462 (36)

MDRRDAMGLSGSG
MDGREAMAFSG

MEAKDVSPLVTVPAPAAAAAPPPAAPPPSQPPPLPFAQQAPPPAA
MDSREIHHQQQQQQQQQQQQQQQQ

MD
MD
MDPVQSH
MDPVTAS
MDPVTAA

FIG. 5A

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G1071	(95)	SYIHRGLSGSGPPTFHGSPQQQQLRHLPNQNSPFGSGSTGFGSPSLHG
T06584	(102)	GPGSYLHRGGVEAAGSGSGGFQVPPGFRALPNNGIIAQPNVRAQGGNGD
SAP1	(103)	MEQPNNDGNNGSCYRPLPNQ-----
G1072	(96)	METSDRISPGGIGAEVPSAYHMAPRPSDS-----
AAK00433	(104)	NPAAAPMRLSFDOMAGKAPGEGEQHHHPGPMLYAAAPAGGAAPPQGGN
G1068	(97)	HLQQQQQPPPGMLMSHHNSYNRNPNAAAVLMGHTSTSQAMHQRLPFGG
G1069	(42)	MANPWTNQSLAGMVDH-----
G2153	(6)	MANPWWTGQVNLSGLETTTPGSSQ--LKKPDLHI
G3456	(14)	MANRWWTGSVGLENGHS-----
G3401	(38)	
G3402	(101)	
G3403	(22)	
G2157	(98)	MGLPEQPSG-----
G3556	(40)	MANPWWVGNVAIGGVESPVTSSAPSLHHRNSNN
G1067	(4)	
G2156	(8)	MEGGEQGGGASRYFHNLFERPEIHQQQLQPQGGINLIDQHHH
G3400	(30)	MDGGYDQSGGASRYFHNLFERPELHHQLQ-PQPQLHPLPQPQP
G3399	(10)	MAGMDPTGGGGGVAHYLHMLRAQQH--QPLSPAGDVKA
G1073	(2)	MAGMDPGGGAGAGSSRYFHLLLRPQQPSPLSPTSHTSHVKM
G2789	(99)	EVS-----RSHTPQFLSSD-HQYHHQNA-----GRQKRGRE-----
G596	(100)	QVS-----RSLPPPFLSRDLHLHPHQFO-----HQQQQQQNHGHDI
G1070	(48)	GSQ-----SSLPPPFFHARDFQLHLQQQQQEFFLHHHQQRNQTGDQQG
G3405	(28)	IHG-----HHLPPPFTTRDFHHLQQQQHQLHLKTEDDQGGTGVFG-
G3404	(32)	AAHGGHHHHFAGPPVAAFHHHPFHGGGAHYPAAFQFQEEQQLVA
G1075	(52)	MAGLDLG-TTSRYVHNVDGG-GGGQFTTDNHHEDDG-----
G1076	(54)	MAGLDLG-TAFRYVNHQLHR-PDLHLHNSSSDDVTP-----
G3460	(18)	MAGLDLG-SASRFVQN-LHL-PDLHLQQNYQQPR-----
G3459	(16)	MAGLDLG-SASRFVQN-LHR-PDLHLQQNYQQHQDQ-----
G3458	(24)	MAGLDLG-SASHFVHRLER-PDLEDENQQDQDNN-----
G3406	(26)	MAGLDLGTAAATRYVHQLHHLHPDLQLQHSYAKQHEP-----
G3407	(34)	MAGLDLG-----TSYLHHHQLHLRHDDGGAG-----MK
G1945	(44)	
G2155	(46)	
G3408	(20)	MSFCERDMNKESMYQERDDMAGIRFATPPLPQQQQQ-----
BAB64709	(105)	
G3462	(36)	

FIG. 5B

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G1071	(95)	DPSLATAAGGAGALPHHIGVNMIA	PPPPSETPMKKRGRPRKYQDGSV	
T06584	(102)	TSSMFSLPEQSHADFNHDI	SVGASSGAPSEPVKKRGRPRKYGPDGSVS	
SAP1	(103)	-----SPANGVPNSTT	TNSTHSPNESVKKRGRPR-----KYGTP	
G1072	(96)	-----PANQFMGLSLP	MEAPMPSSGEASGKKRRGRPR-----YEANGA	
AAK00433	(104)	VMGMELMRKKRGRPRKYA	PDGSMALALAPISSASGGAAPPPPPGHQPH	
G1068	(97)	SMSPHQPQQHQYHHPQ	QQQIDQKTLESIGFTSPLPSASNSYGGNEG	
G1069	(42)	-----SVSSGHHQNH	HHQSLTKGDLGIAMNQSDNDQDE-----EDDPR	
G2153	(6)	SMNMAMDSGHNHHH	QEVNNDNN-----DDDRDNLSGD-----DHEPR	
G3456	(14)	-----MKK-PDLGFS	MNESTVTGNHIG-----EDEDRENSD-----EPR	
G3401	(38)	MASKEPSG	-----DHDHEMNGTSAG-----GGEPK	
G3402	(101)	MASKEPSGDH	-----DHDHEMNGTSAG-----GGEPK	
G3403	(22)	-----SSGPKAELP	VAKEPEASPTGGA-----AADHADENNESG-----GGEPR	
G2157	(98)	NPPTMTRSDPRLDH	FTTNNSGSPNTQTQSQEEQNSRDE-----QPAVE	
G3556	(40)	MGSIDGHSLOQH	QGYSHGGAGGSENEEASPPP-----GGGSA	
G1067	(4)	QHQQHQQQ	QPSDDSR-----ESDSNKDHHQQG-----RPDS	
G2156	(8)	QPQPQQN	-----SDD-----ESDS-NKD-----PGSD	
G3400	(30)	ERSMLSPDES	PGADAD-----LGSDH-PTSSAMVA-----AED-S	
G3399	(10)	EHSKMSPDKSPV	GEGDHAGSGSGVGGDHQPSSSAMVP-----VEGGS	
G1073	(2)	MELNRSEADEAK	-----AETPTGGATSS-----ATA--	
G2789	(99)	-----EEGVEPN	-----NIGEDLATFPSSG-----EE--	
G596	(100)	DQHRIGGLKRDR	-----DADIDPNEHSSAGKDQSTPGSG-----GESGG	
G1070	(48)	GSGGNROI	KMDREETSDNIDNIANNSGSEKDDIHGGS-----GEGGG	
G3405	(28)	-----SRGTRKD	HDD--DENSGNHGSGGDDGDLALVPPS-----GGGPD	
G3404	(32)	AAAAAGGMAKQEL	VDESNTINSGSGNSGGEQRQSG-----EEQH	
G1075	(52)	-----GAGGNHHH	--HHNHHHQQGLDLIASNDN-SG-----LGCGG	
G1076	(54)	-----GAGMGHFT	VDDENNNNHQQGLDLASGGSGSS-----GGGGG	
G3460	(18)	-----HKRDSE	EQETPPNPGTALAPFDND-DDKS-----QGLEL	
G3459	(16)	-----QHQRDL	EEQKTPPN-HRMGAPFDDDDSDRS-----PGLLEL	
G3458	(24)	-----LNNHEGLD	LVTNPS-----G-----G--	
G3406	(26)	-----SDDDPNGS	GCGGNSNGGPYGDHDDGSSSSSGP-----ATDGA	
G3407	(34)	-----SDDGGH	DDLSPGS-----GGGGPSS-----TAGGA	
G1945	(44)	GEYREQS	NEMFSLPHHQQQQQQQHSLTSHFHLSS-----TVTPT	
G2155	(46)	MLSKLPTQR	-----HLHLSP-----SSP--	
G3408	(20)	-----QQLVEC	FSDEVDSRSGGGE--MKDAVGS	SGQLV-----VVG
BAB64709	(105)	MADEGSSRAELI	-----EASPA	
G3462	(36)	TRSNSNTNANTNTNT	TTEEEVSRDNGEDQNQLGS-----HEGSE	

FIG. 5C

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G1071	(95)	SLALSSSSVSTITPNN	--SNKR	--GRGRPPGSGKK	--QRMASV	GELMPSS	
T06584	(102)	LKLTPMSAPANSTQDSGTPSEKR	--GRGRPPGSGKK	--GRGRPPGSGKK	--QOLAAL	GDWMTSS	
SAP1	(103)	EQAAAARKRLS	--APKKRDS	AGVAVSS	SSKSP	IAALGN	
G1072	(96)	PLP-SSSVPL	--VKKR	--VRGKLNG	EDMK	--KMHKTI	GFHSSGE
AAK00433	(104)	GFSISSPASD	--PNAK	--RRGRPPGSGKK	--KQFEAL	GSWG	--
G1068	(97)	GGGDSAGANANSSD	--PPAKR	--NRGRPPGSGKK	--OLDAL	GGTG	--
G1069	(42)	EGA--VEVV	--NRR	--PRGRPPGSGKNK	--PKAPI	EFVTRD	--
G2153	(6)	E--GAVEAP	--TRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3456	(14)	E--GAIDVA	--TTR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3401	(38)	D--GAVVTG	--RNRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3402	(101)	D--GAVVTG	--RNRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3403	(22)	E--GAVVAA	--PNRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G2157	(98)	P--GSGSGS	--TGRR	--PRGRPPGSGKNK	--PKSPVV	VTKE	--
G3556	(40)	T--GS--	--AGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1067	(4)	PN--TSSSA	--PGKR	--PRGRPPGSGKNK	--AKPPI	EFVTRD	--
G2156	(8)	P--VTSGS	--TGKR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3400	(30)	G--GSGSGG	--PMRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3399	(10)	GSAGGSGSGG	--PTRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1073	(2)	S--GSSG	--RR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G2789	(99)	--NI	--KKRR	--PRGRPPGSGKNK	--PKAPI	EFVTRD	--
G596	(100)	G--GGDNH	--ITRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1070	(48)	G--SGDHO	--MTRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3405	(28)	G--AGS-ES	--ATTR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3404	(32)	Q--GAAAPV	--VIRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1075	(52)	G--GSGDL	--VMRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1076	(54)	H--GGGDV	--VGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3460	(18)	A--SGPGDI	--VGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3459	(16)	T--SGPGDI	--VGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3458	(24)	--PGDV	--VGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3406	(26)	V--GGPDV	--VARR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3407	(34)	G--IGGEV	--VARR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G1945	(44)	V--DDSSIE	--VVR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G2155	(46)	--SME	--TVGR	--PRGRPPGSGKNK	--PKAPI	EFVTRD	--
G3408	(20)	D--GASIE	--VAKK	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
BAB64709	(105)	P--ALDLP	--PPRK	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--
G3462	(36)	P--GS	--SGRR	--PRGRPPGSGKNK	--PKPPI	EFVTRD	--

AT-hook domain

FIG. 5D

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G1071	(95)	SGMSFTPHVIAVSLIGEDIASKVIAFSQOQGPRAICVLSAS
T06584	(102)	AGLAFSPHVIITIAAGEDIAAKLLLSQORRALCILSGT
SAP1	(103)	MGQSFSPHIIITVAAGEDVQKIMMFVQOSKREICVISAS
G1072	(96)	RFGVGGVGGVSNFTPHVITMNTGEDITMRISFSQOQGPRAICILSAN
AAK00433	(104)	IAFTPHIILTMKAGEDVASKIMAFSQOQGPRTVCILSAN
G1068	(97)	GVGFTPHVIEVKITGEDIAATKILAFNQGPRAICILSAT
G1069	(42)	SPNALRSHVLEISDGSADVADTIAHFSRRRQRGVCVLSGT
G2153	(6)	SPNALKSHVMEIASGTDVIEETLAFARRRQRGICILSGN
G3456	(14)	SPNALRSHVMEIAVGDVADCVAQFARRRQRGVSILSGS
G3401	(38)	SPNALRSHVMEVAGCADVAESIAHFARRRQRGVCVLSGA
G3402	(101)	SPNALRSHVMEVAGCADVAESIAHFARRRQRGVCVLSGA
G3403	(22)	SPNALRSHVMEVAGCADVAESIAHFARRRQRGVCVLSGA
G2157	(98)	SPNSLQSHVLEIATGADVAAESINAFARRRQRGVSILSGS
G3556	(40)	SPNAMRSHVLEIASGADIIEAIAGFARRRQRGVSILSGS
G1067	(4)	SPNALRSHVLEVSFGADIIVESVTYARRRQRGVSILSGN
G2156	(8)	SPNMLRSHVLEVSFGADIIVESVTYARRRQRGVSILSGN
G3400	(30)	SPNAFHSHVLEVAAGTDIIVESVTFARRRQRGVSILSGG
G3399	(10)	SPNALHSHVLEVAAGTDIIVESVTFARRRQRGVSILSGG
G1073	(2)	SPNMLRSHVLEVTSGSDIIEAVSTYARRRQGVCIISGT
G2789	(99)	SANAFRCHVMEITINACDVMEESLAFARRRQRGVCVLTGN
G596	(100)	SANALKSHVMEVANGCDVMEESVTFARRRQRGICVLSGN
G1070	(48)	SANALRTHVMEIGDGCDDLVESVATFARRRQRGVCMST
G3405	(28)	SANTLRTHVMEVAGGCCDIIESITTFARRRQRGVCVLSGA
G3404	(32)	SASALRAHVLEVASGCCDLVDSVATFARRRQVGVCLSAT
G1075	(52)	SANTLRAHILEVSGGCCDVFEICISTYARRRQRGICVLSGT
G1076	(54)	SANTLRAHILEVINGCCDVFD CVATYARRRQRGICVLSGS
G3460	(18)	SANTLRAHILEVSGSDVFD CVTA YARRRQRGICVLSGS
G3459	(16)	SANTLRAHILEVSGSDVFD CVTA YARRRQRGICVLSGS
G3458	(24)	SANTLRAHILEVSSGCCDVFEESVATYARRRQRGICVLSGS
G3406	(26)	SANTLRAHILEVSGGCCDVFEESVATYARRRQRGICVLSGS
G3407	(34)	SANALRAHILEVAAGCCDVFEALTA YARRRQRGVCVLSA
G1945	(44)	IDPHMSPYILEVPSGNDVMEAINRFCRRKSTGVCVLSGS
G2155	(46)	IDPHMSPYILEVPSGNDVMEAINRFCRRKSTGVCVLSGS
G3408	(20)	PAAAMRPHVIEIPGGRDVAEALRFSRRNLGICVLAGT
BAB64709	(105)	SEAMRPVVLELGA GCEVA AVAAFAARRRQGVSVLCCR
G3462	(36)	SPNALRSHVLEIASGRDVAFESIAAFANRRHRGVSVLSGS

second conserved domain

FIG. 5E

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G1071	(95)	GAVSTATLILQP	---	SASPG	---	ATKVEGRFEILALS	---	TSYIVATDG	---
T06584	(102)	GIASKVTLRQP	---	ASTNAG	---	VTVYEGKFOILSLSGSYLVSEDDG	---		---
SAP1	(103)	GSVSSALRQP	---	ASSGG	---	SVTVYEGRFDILSLSGSFIHAE	---		---
G1072	(96)	GVISNVTLRQP	---	DISCGG	---	TLTVYEGRFEILSLSGSFMETENQG	---		---
AAK00433	(104)	GAI SNVTLRQP	---	ATS	---	LVTVYEGRFEILSLSGSFLAEDGD	---		---
G1068	(97)	GAVTNMMLRQAN	---	NSNPTG	---	TVKYEGRFEILSLSGSFLNSESNG	---		---
G1069	(42)	GSVANVTLRQ	---	AAAPGG	---	VVSLQGRFEILSLTGAFLLPCE	---		---
G2153	(6)	GTVANVTLRQP	STAA	VAAAPGGAA	---	VVALQGRFEILSLTGSLPCE	---		---
G3456	(14)	GTVNVTLRQP	---	TAPGAV	---	MALHGRFDILSLTGSLPCE	---		---
G3401	(38)	GTVIDVALROP	---	AAPSA	---	VVALRGRFEILSLTGTFLLPCE	---		---
G3402	(101)	GTVIDVALROP	---	AAPSA	---	VVALRGRFEILSLTGTFLLPCE	---		---
G3403	(22)	GTVANVALROP	---	SAPGA	---	VVALHGRFEILSLTGTFLLPCE	---		---
G2157	(98)	GLVTNVTLRQ	AAS	---	GG	VVSLRQGRFEILSMCGAFLPTSG	---		---
G3556	(40)	GAVTNVTLRQ	AGTG	---	AA	AVALRGRFEILSMCGAFLPAP	---		---
G1067	(4)	GTVSNVTLRQP	VTPGNGGVSG	GGG	---	VVTLHGRFEILSLTGTVLPP	---		---
G2156	(8)	GTVANVTLRQP	ATTAHANG	GGG	---	VVALHGRFEILSLTGTVLPP	---		---
G3400	(30)	GAVANVTLRQP	G	---	ASPPGSL	VATMRGRFEILSLTGTVLPP	---		---
G3399	(10)	GAVNVTLRQP	G	---	ASPPGSM	VATLRGRFEILSLTGTVLPP	---		---
G1073	(2)	GAVTNVTIROP	---	AAPAGG	---	VITLHGRFDILSLTGTVLPP	---		---
G2789	(99)	GAVTNVTIROP	---	PGG	---	VVSLHGRFEILSLSGSFLPP	---		---
G596	(100)	GAVTNVTIROP	AS	---	VPGGS	VVNLHGRFEILSLSGSFLPP	---		---
G1070	(48)	GNVTNVTIROP	GS	---	HPS	VVSLHGRFEILSLSGSFLPP	---		---
G3405	(28)	GTVTNVTLRQ	---	PASQGA	---	VVALHGRFEILSLSGSFLPP	---		---
G3404	(32)	GAVTNVSVROP	---	GAGPGA	---	VVNLHGRFDILSLSGSFLPP	---		---
G1075	(52)	GTVTNVTIROP	---	TAAGA	---	VVTLRGTTFEILSLSGSFLPP	---		---
G1076	(54)	GTVTNVTIROP	---	SAAGA	---	VVTLQGTTFEILSLSGSFLPP	---		---
G3460	(18)	GTVTNVTIROP	---	AAAGA	---	VVRLHGRFEILSLSGSFLPP	---		---
G3459	(16)	GTVTNVTIROP	---	AAAGA	---	VVTLHGRFEILSLSGSFLPP	---		---
G3458	(24)	GTVTNVTIROP	S	---	AAAGA	VVTLHGRFEILSLSGSFLPP	---		---
G3406	(26)	GNVTNVTLRQ	S	---	APAGA	VVSLHGRFEILSLSGSFLPP	---		---
G3407	(34)	GTVANVTLRQP	QSAQ	PGPASEA	---	VATLHGRFEILSLAGSFLPP	---		---
G1945	(44)	GSVANVTLRQ	S	---	PAALGS	TTTFHKGFDLLSVSATFLPP	PPTS		
G2155	(46)	GSVANVTLRQ	S	---	PAAPGS	TTTFHKGFDLLSVSATFLPP	PPTS		
G3408	(20)	GAVANVTLRHSP	---	GVPGSAP	---	PAIVFHGRYEILSLSATFLP	AMSSV		
BAB64709	(105)	GTVAVTLRQP	---	TSPPA	---	AVKLHGRFEVLSLSTGTVLPS	AAGEG		
G3462	(36)	GTVANVTLRQ	AAP	---	AG	VITLHGRFEILSLSGAFLP	SE		

second conserved domain

FIG. 5F

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G1071 (95)
T06584 (102)
SAP1 (103)
G1072 (96)
AAK00433 (104)
G1068 (97)
G1069 (42)
G2153 (6)
G3456 (14)
G3401 (38)
G3402 (101)
G3403 (22)
G2157 (98)
G3556 (40)
G1067 (4)
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G3406 (26)
G3407 (34)
G1945 (44)
G2155 (46)
G3408 (20)
BAB64709 (105)
G3462 (36)

--SFRNRITGNLSVSLASPDGRVIGGAI GGPLIAASPVI VVGSFI--WAAP
--PTNRITGGLSVLSLRDGHVIGGSVA-MLIAGSPIQLVVCSEFV-YGGG
--FGGRITGGLSVLSLRDGOIIGGVGGPILIAAATIQVIVGTFFV-VETIK
--SKGRITGGLSVLSLAGPDGRVVGCGVAGLLIAATPIQVIVGSFI-TSDQ
--TRSRITGGLSVLSLAGSDGRVLGCGVAGMLMAATPVQVIVASFI-AEGK
--TVTKITGNLSVSLAGHEGRIVGCGVDGMLVAGSQVQVIVGSFVPDGRK
--SPPGSTGLTVYLAGVQGOVVGGSVVGPLLAIGSVMI AATFS-NATY
--APPGSTGLTVYLAGGQGOVVGGSVVGPLMAAGPVM LIAATFS-NATY
--SPPGATGLTVYLAGGQGOVVGGSVVGPLV AAGPVLVMAATFS-NATY
--APPGSTGLTVYLAGGQGOVVGGSVVGTLT AAGPVMVIASTFA-NATY
--APPGSTGLTVYLAGGQGOVVGGSVVGSLI AAGPVMVIASTFA-NATY
--SPPAAGLTVYLAGAQGOVVGGSVVGAGPLI AAGPVMVIAATFC-NATY
--APPGATGLAVYLAGGQGOVVGGSVVGELI AAGPVMVIAATFG-NATY
--APPGAGGLSIFLAGGQGOVVGGSVVGAPLI AAGPVLMAASF-NATY
--APPGSGGLSIFLSGMOGOVIGGNVAPLVA SGPVLMAASF-NATY
--APPSASGLTVFLSGGQGOVVGGSVVGQOL I AAGPVLMAASF-NATY
--APPGASGLTVFLSGGQGOVVGGSVVGSLI AAGPVLMAASF-NATY
--APPGAGGLTVYLAGGQGOVVGGSVVGNA GSPVVMMAASF-NATY
--APPAASGLTVYLAGGQGOVVGGSVVGPLT AAGPVLMAASF-NATY
--APPAASGLTVYLAGGQGOVVGGSVVGPLM AAGPVLMAASF-NATY
--APPTATGLSVYLAGGQGOVVGGSVVGPLLC AGPVLMAASF-NATY
--APPEATGLTVYLAGGQGOVVGGSVVGAL T AAGPVLMAASF-NATY
--APPSATGLTVYVSGGQGOVVGGSVVGELM AAGPVLMAASF-NATY
--APPGATSLTIFLAGAQGOVVGGSVVGELM AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGELT AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGELT AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGELT AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGELT AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGELT AAGPVLMAASF-NATY
--APPGATSLTIFLAGGQGOVVGGSVVGAL I AAGPVLMAASF-NATY
--APPGATSLAFLAGGQGOVVGGSVVGAGAL I AAGPVLMAASF-NATY
L--SPPVSNFTVLSLAGPQGOIIGGFVAGPLI SAGTVMVIAASF-NATY
L--SPEVSNFTVLSLAGPQGVIGGFVAGPLV AAGTVMVIAATSF-NATY
APQA AAVAAGLSISLAGPHGOIVGGAVAGPLI YAAITVMVIAAATF-NATY
A--APPPP--FVSISLAGAGGOVIGGTLAGE MTTADGLVVAATFG-SAEV
--SPPGATGLTVYLAGGQGOVVGGSVVGSLV ASGPVMVIAATFG-NATY

second conserved domain

FIG. 5G

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G1071	(95)	KIKSKKR	EE	---	ASEVVOETD	---	DHHVLDNNN	---	NT
T06584	{102}	SKVKTKQ	---	---	MITNGES	---	SEPHNDNLG	---	SPASA
SAP1	{103}	KDANVEAAS	---	---	GKSPSPNGG	---	ASAPGLSFRSPADSGIOM	---	
G1072	(96)	QDHQKPRKR	---	---	VEHAPAAVMS	---	VPPPPSPPPAASVFSPT	---	
AAK00433	{104}	KSKPVEVTRKVEP	---	---	MSAPPOMATYVPAPVASPPSEGT	---	---	---	SGS
G1068	(97)	QKOSAGRAQN	---	---	TPEPASAPANMLSF	---	GGPGSPRSQ	---	QOHSSE
G1069	{42}	ERLPMEEE	---	---	E-DGGCSR	---	QIHGGDSPP	---	RIGSNL
G21053	(6)	ERLPLEEEFAA	---	---	ERGGGCGSGGVVPGL	---	GGG-SPL	---	SSGAGG
G3456	{14}	ERLPLEDD	---	---	DQEQHCGG	---	GGSP-QE	---	KNGGPG
G3401	{38}	ERLPDQEE	---	---	EEEAAG	---	GMMAPPP	---	LMAG--
G3402	(101)	ERLPDQED	---	---	QEEAAG	---	GMMAPPP	---	LMAG--
G3403	{22}	ERLPLEEE	---	---	EEGSGPP	---	MPGGAEP	---	LMAGGH
G2157	{98}	ERLPLEEEQ	Q	---	QEQPLOED	---	GKKQKEEND	---	NESGNN
G3556	{40}	ERLPDQEE	E	---	EGAVLSGSE	---	GAAQOMEQ	---	SS
G1067	{4}	ERLPLEEE	---	---	EEGGCG	---	GGG-GGPPQM	---	QAPSASPP
G2156	{8}	ERLPLE-DEG	---	---	EGEGCGEVGE	---	GGG-GGPPQM	---	PATSSSPP
G33400	{30}	ERLPDGEDPE	---	---	AEAAATPPGDAAQPT	---	GGG-GGPPQM	---	PATSSSPP
G33399	{10}	ERLPLEGE	---	---	VAAPAAAGEADQVAQ	---	GGG-GGPPQM	---	PATSSSPP
G1073	{2}	ERLPLEEE	---	---	TPPRTTGVQQQ	---	GGG-GGPPQM	---	PATSSSPP
G2789	{99}	ERLPLEEE	---	---	TEREIDGNA	---	GGG-GGPPQM	---	PATSSSPP
G596	{100}	ERLPLEEDQ	---	---	EEQTAGAVANNIDGNA	---	GGG-GGPPQM	---	PATSSSPP
G1070	{48}	ERLPLEED	---	---	MQTPVHCGG	---	GGG-GGPPQM	---	PATSSSPP
G3405	{28}	ERLPLEED	---	---	LLAAQQA	---	GGG-GGPPQM	---	PATSSSPP
G3404	{32}	ERLPLEED	---	---	PPQHMA	---	GGG-GGPPQM	---	PATSSSPP
G1075	{52}	ERLPLEDEH	---	---	LQSGGG	---	GGG-GGPPQM	---	PATSSSPP
G1076	{54}	ERLPLEED	---	---	QQLGGSN	---	GGG-GGPPQM	---	PATSSSPP
G3460	{18}	ERLPLEED	---	---	HQQLQIQSPAATS	---	GGG-GGPPQM	---	PATSSSPP
G3459	{16}	ERLPLEED	---	---	QQLQIQPPATTS	---	GGG-GGPPQM	---	PATSSSPP
G3458	{24}	ERLPLEED	---	---	SMQMQGSSAGDGS	---	GGG-GGPPQM	---	PATSSSPP
G3406	{26}	ERLPLEED	---	---	APPOAGLQMQPGGA	---	GGG-GGPPQM	---	PATSSSPP
G3407	{34}	ERLPLEED	---	---	VPPAPAGSDQGGGS	---	GGG-GGPPQM	---	PATSSSPP
G1945	{44}	ERLPLEED	---	---	HSAGTGER	---	GGG-GGPPQM	---	PATSSSPP
G2155	{46}	ERLPLEED	---	---	RNSAEGEE	---	GGG-GGPPQM	---	PATSSSPP
G3408	{20}	ERLPLEED	---	---	VSVSLSGSG	---	GGG-GGPPQM	---	PATSSSPP
BAB64709	{105}	ERLPLEED	---	---	ATGSRGEE	---	GGG-GGPPQM	---	PATSSSPP
G3462	{36}	ERLPLEED	---	---	EEMVQVQQQ	---	GGG-GGPPQM	---	PATSSSPP

FIG. 5H

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[illegible]

FIG. 5I

Protein	Position	Sequence
G1071	(95)	NRHDS
T06584	(102)	NSPQ
SAP1	(103)	RP
G1072	(96)	RP
AAK00433	(104)	RP
G1068	(97)	RP
G1069	(42)	RP
G2153	(6)	RP
G3456	(14)	RP
G3401	(38)	RP
G3402	(101)	RP
G3403	(22)	RP
G2157	(98)	RP
G3556	(40)	RP
G1067	(4)	RP
G2156	(8)	RP
G3400	(30)	RP
G3399	(10)	RP
G1073	(2)	RP
G2789	(99)	RP
G596	(100)	RP
G1070	(48)	RP
G3405	(28)	RP
G3404	(32)	RP
G1075	(52)	RP
G1076	(54)	RP
G3460	(18)	RP
G3459	(16)	RP
G3458	(24)	RP
G3406	(26)	RP
G3407	(34)	RP
G1945	(44)	RP
G2155	(46)	RP
G3408	(20)	RP
BAB64709	(105)	RP
G3462	(36)	RP

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